

## AMENDMENTS TO THE SPECIFICATION

*Please insert the following paragraph at page 1, immediately following the title:*

This is a U.S. National Stage Application under 35 U.S.C. § 371 of International Patent Application No. PCT/FR2005/000070, filed January 12, 2005, which claims priority to French Patent Application No. 0400214, filed January 12, 2004. The contents of both applications are incorporated in their entirety by reference.

*Please replace the paragraph at page 7, lines 13 to 20 with the following amended paragraph:*

The means of identification of the homologous sequences and their percentage homologies are well-known to those skilled in the art, and include in particular the BLAST programmes that can be used on the ~~website <http://www.ncbi.nlm.nih.gov/BLAST/> with website [ncbi.nlm.nih.gov/BLAST/](http://www.ncbi.nlm.nih.gov/BLAST/), with~~ the default parameters indicated on that website. The sequences obtained can be exploited (aligned) using for example the programmes ~~CLUSTALW (<http://www.ebi.ac.uk/clustalw/>) or MULTALIN (<http://prodes.toulouse.inra.fr/multalin/cgi-bin/multalin.pl>)~~, CLUSTALW ([ebi.ac.uk/clustalw/](http://www.ebi.ac.uk/clustalw/)) or MULTALIN ([prodes.toulouse.inra.fr/multalin/cgi-bin/multalin.pl](http://prodes.toulouse.inra.fr/multalin/cgi-bin/multalin.pl)), with the default parameters indicated on these websites.

*Please replace the paragraphs at page 10, lines 18 to 27 with the following amended paragraphs:*

The PFAM database (protein families database of alignments and hidden Markov ~~models~~ <http://www.sanger.ac.uk/Software/Pfam/>) ~~is~~ [models, sanger.ac.uk/Software/Pfam/](http://www.sanger.ac.uk/Software/Pfam/)) is a large collection of alignments of protein sequences. Each PFAM makes it possible to visualise multiple alignments, view protein domains, evaluate distributions among organisms, gain access to other databases and visualise known protein structures.

COGs (clusters of orthologous groups of ~~proteins~~ <http://www.ncbi.nlm.nih.gov/COG/>) ~~are~~ [proteins, ncbi.nlm.nih.gov/COG/](http://www.ncbi.nlm.nih.gov/COG/)) are obtained by comparing protein sequences derived from 43 fully sequenced genomes representing 30 major phylogenetic lines. Each COG is defined from at least three lines, making it possible to identify ancient conserved domains.

*Please replace the paragraph at page 14, lines 15 to 22 with the following amended paragraph:*

The present invention leads advantageously to the selection of mutations of the gene *lpd* (the wild sequence of which is known: ~~<http://genolist.pasteur.fr/Colibri>~~) coding known: [genolist.pasteur.fr/Colibri](http://genolist.pasteur.fr/Colibri)) coding for the lipoamide dehydrogenase of the pyruvate dehydrogenase complex. In particular, the presence of a point mutation causing the replacement of alanine 55 by a valine has been identified. This enzyme is known to be responsible for the inhibition of the pyruvate dehydrogenase complex by NADH. This modified enzyme is also an object of the present invention.

*Please replace the paragraph at page 16, lines 4 to 6 with the following amended paragraph:*

- a region (lower-case letters) homologous to the sequence (4109007-4109087) of the gene *tpiA* (sequence 4108320 to 4109087), a reference sequence on the website ~~<http://genolist.pasteur.fr/Colibri/>~~, and [website genolist.pasteur.fr/Colibri/](http://genolist.pasteur.fr/Colibri/), and

*Please replace the paragraph at page 17, lines 20 to 23 with the following amended paragraph:*

- a region (lower-case letters) homologous to the sequence (952235-952315) of the gene *plfB* (sequence 950495 to 952777), a reference sequence on the website ~~<http://genolist.pasteur.fr/Colibri/>~~, and [website genolist.pasteur.fr/Colibri/](http://genolist.pasteur.fr/Colibri/), and

*Please replace the paragraph at page 20, lines 17 to 19 with the following amended paragraph:*

- a region (lower case letters) homologous to the sequence (1297263-1297343) of the gene *adhE* (sequence 1294669 to 1297344), a reference sequence on the site ~~<http://genolist.pasteur.fr/Colibri/>~~, and [site genolist.pasteur.fr/Colibri/](http://genolist.pasteur.fr/Colibri/), and

*Please replace the paragraph at page 23, lines 1 to 3 with the following amended paragraph:*

- a region (lower case letters) homologous to the sequence (1725861-1725941) of the gene *gloA* (sequence 1725861 to 1726268), reference sequence on the website ~~<http://genolist.pasteur.fr/Colibri/>~~, and [website genolist.pasteur.fr/Colibri/](http://genolist.pasteur.fr/Colibri/), and

*Please replace the paragraph at page 24, lines 23 to 25 with the following amended paragraph:*

- a region (lower case letters) homologous to the sequence (1486256-1486336) of the gene *aldA* (sequence 1486256 to 1487695), reference sequence on the ~~website <http://genolist.pasteur.fr/Colibri/>~~, and website [genolist.pasteur.fr/Colibri/](http://genolist.pasteur.fr/Colibri/), and

*Please replace the paragraph at page 26, lines 14 to 16 with the following amended paragraph:*

- a region (lower case letters) homologous to the sequence (3752603-3752683) of the gene *aldB* (sequence from 3752603 to 3754141), reference sequence on the ~~website <http://genolist.pasteur.fr/Colibri/>~~, and website [genolist.pasteur.fr/Colibri/](http://genolist.pasteur.fr/Colibri/), and

*Please replace the paragraph at page 31, lines 4 to 6 with the following amended paragraph:*

- a region (lower case letters) homologous to the sequence (4135512 to 4135592) of the gene *gldA* (sequence 4135512 to 4136615), reference sequence on the ~~website <http://genolist.pasteur.fr/Colibri/>~~, and website [genolist.pasteur.fr/Colibri/](http://genolist.pasteur.fr/Colibri/), and

*Please replace the paragraph at page 34, lines 5 to 7 with the following amended paragraph:*

- a region (lower case letters) homologous to the sequence (1930817 to 4) of the gene *edd* (sequence 1930817 to 1932628), reference sequence on the ~~website <http://genolist.pasteur.fr/Colibri/>~~, and website [genolist.pasteur.fr/Colibri/](http://genolist.pasteur.fr/Colibri/), and